R. Schuadron

1644

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 08/01/2000
PATENT APPLICATION: US/09/248,964   TIME: 13:05:48

Input Set : A:\HAR005.APP.app
Output Set: N:\CRF3\08012000\I248964.raw

```
 3 <110> APPLICANT: WUCHERPFENNIG, Kai W
 4         STROMINGER, Jack L
 6 <120> TITLE OF INVENTION: MONOVALENT, MULTIVALENT AND MULTIMERIC MHC BINDING
 7         DOMAIN FUSION PROTEINS AND CONJUGATES, AND USES
 8         THEREFOR
.10 <130> FILE REFERENCE: HAR-005
12 <140> CURRENT APPLICATION NUMBER: 09/248,964
13 <141> CURRENT FILING DATE: 1999-02-12
15 <150> PRIOR APPLICATION NUMBER: PCT/US97/14503
16 <151> PRIOR FILING DATE: 1997-08-15
18 <150> PRIOR APPLICATION NUMBER: 60/075,351
19 <151> PRIOR FILING DATE: 1998-02-19
21 <150> PRIOR APPLICATION NUMBER: 60/024,007
22 <151> PRIOR FILING DATE: 1996-08-15
24 <160> NUMBER OF SEQ ID NOS: 14
26 <170> SOFTWARE: PatentIn Ver. 2.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 750
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Description of Artificial Sequence: DR2-Fos fusion
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (1)..(735)
40 <220> FEATURE:
41 <221> NAME/KEY: misc_feature
42 <222> LOCATION: (1)..(21)
43 <223> OTHER INFORMATION: 3' end of secretory signal
45 <220> FEATURE:
46 <221> NAME/KEY: misc_structure
47 <222> LOCATION: (22)..(594)
48 <223> OTHER INFORMATION: DRA*0101 extracellular domain
50 <220> FEATURE:
51 <221> NAME/KEY: misc_feature
52 <222> LOCATION: (595)..(615)
53 <223> OTHER INFORMATION: Linker sequence
55 <220> FEATURE:
56 <221> NAME/KEY: misc_feature
57 <222> LOCATION: (616)..(735)
58 <223> OTHER INFORMATION: Fos leucine zipper domain
60 <400> SEQUENCE: 1
61 gta tct ctc gag aaa aga gag atc aaa gaa gaa cat gtg atc atc cag    48
62 Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
63   1               5                  10                  15
65 gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac    96
66 Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
```

RAW SEQUENCE LISTING   DATE: 08/01/2000
PATENT APPLICATION: US/09/248,964   TIME: 13:05:48

Input Set : A:\HAR005.APP.app
Output Set: N:\CRF3\08012000\I248964.raw

```
67  ·              20              25              30
69 ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg  144
70 Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
71              35              40              45
73 gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa  192
74 Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
75       50              55              60
77 ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa atc atg  240
78 Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
79 65              70              75              80
81 aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta  288
82 Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
83              85              90              95
85 act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc  336
86 Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
87              100             105             110
89 atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc acg tgg  384
90 Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
91       115             120             125
93 ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca gtc ttc  432
94 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
95       130             135             140
97 ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cat tat ctc ccc ttc  480
98 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
99 145             150             155             160
101 ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac tgg ggc  528
102 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
103             165             170             175
105 ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca agc cct  576
106 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
107             180             185             190
109 ctc cca gag act aca gag gtc gac gga ggt ggc ggc ggt tta act gat  624
110 Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp
111       195             200             205
113 aca ctc caa gcg gag aca gat caa ctt gaa gac gag aag tct gcg ttg  672
114 Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
115       210             215             220
117 cag acc gag att gcc aat cta ctg aaa gag aag gaa aaa ctg gag ttc  720
118 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
119 225             230             235             240
121 atc ctg gcc gcc cat tgagaattct atgac                           750
122 Ile Leu Ala Ala His
123             245                                    \
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 245
128 <212> TYPE: PRT
129 <213> ORGANISM: Artificial Sequence
13  <220> FEATURE:
1 1 <223> OTHER INFORMATION:
```

W--> 13
W--> 1 1

see item 7 on Err Summary Sheet

```
                 RAW SEQUENCE LISTING                 DATE: 08/01/2000
                .PATENT APPLICATION:  US/09/248,964   TIME: 13:05:48

                 Input Set : A:\HAR005.APP.app
                 Output Set: N:\CRF3\08012000\I248964.raw
```

```
131 <400> SEQUENCE: 2
132 Val Ser Leu Glu Lys Arg Glu Ile Lys Glu Glu His Val Ile Ile Gln
133   1               5                  10                  15
135 Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp
136              20                  25                  30
138 Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr
139          35                  40                  45
141 Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln
142      50                  55                  60
144 Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met
145   65                  70                  75              80
147 Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val
148              85                  90                  95
150 Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu
151              100                 105                 110
153 Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr Trp
154          115                 120                 125
156 Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr Val Phe
157      130                 135                 140
159 Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu Pro Phe
160 145                 150                 155                 160
162 Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His Trp Gly
163              165                 170                 175
165 Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro
166              180                 185                 190
168 Leu Pro Glu Thr Thr Glu Val Asp Gly Gly Gly Gly Gly Leu Thr Asp
169          195                 200                 205
171 Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys Ser Ala Leu
172      210                 215                 220
174 Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
175 225                 230                 235                 240
177 Ile Leu Ala Ala His
178                  245
181 <210> SEQ ID NO: 3
182 <211> LENGTH: 771
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence: DR@-Jun fusion
189 <220> FEATURE:
190 <221> NAME/KEY: CDS
191 <222> LOCATION: (1)..(756)
193 <220> FEATURE:
194 <221> NAME/KEY: misc_feature
195 <222> LOCATION: (1)..(21)
196 <223> OTHER INFORMATION: 3' end of sectetory signal
198 <220> FEATURE:
199 <221> NAME/KEY: misc_feature
200 <222> LOCATION: (22)..(615)
```

RAW SEQUENCE LISTING   DATE: 08/01/2000
PATENT APPLICATION: US/09/248,964   TIME: 13:05:48

Input Set : A:\HAR005.APP.app
Output Set: N:\CRF3\08012000\I248964.raw

```
201 <223> OTHER INFORMATION: DRB1*1501 extracellular domain
203 <220> FEATURE:
204 <221> NAME/KEY: misc_feature
205 <222> LOCATION: (616)..(636)
206 <223> OTHER INFORMATION: Linker sequence
208 <220> FEATURE:
209 <221> NAME/KEY: misc_feature
210 <222> LOCATION: (637)..(756)
211 <223> OTHER INFORMATION: Jun leucine zipper domain
213 <400> SEQUENCE: 3
214 gta tct ctc gag aaa aga gag ggg gac acc cga cca cgt ttc ctg tgg      48
215 Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp
216   1               5                  10                  15
218 cag cct aag agg gag tgt cat ttc ttc aat ggg acg gag cgg gtg cgg      96
219 Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
220              20                  25                  30
222 ttc ctg gac aga tac ttc tat aac cag gag gag tcc gtg cgc ttc gac     144
223 Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
224          35                  40                  45
226 agc gac gtg ggg gag ttc cgg gcg gtg acg gag ctg ggg cgg cct gac     192
227 Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
228      50                  55                  60
230 gct gag tac tgg aac agc cag aag gac atc ctg gag cag gcg cgg gcc     240
231 Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
232  65                  70                  75                  80
234 gcg gtg gac acc tac tgc aga cac aac tac ggg gtt gtg gag agc ttc     288
235 Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
236                  85                  90                  95
238 aca gtg cag cgg cga gtc caa cct aag gtg act gta tat cct tca aag     336
239 Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
240                 100                 105                 110
242 acc cag ccc ctg cag cac cac aac ctc ctg gtc tgc tct gtg agt ggt     384
243 Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
244             115                 120                 125
246 ttc tat cca ggc agc att gaa gtc agg tgg ttc ctg aac ggc cag gaa     432
247 Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
248     130                 135                 140
250 gag aag gct ggg atg gtg tcc aca ggc ctg atc cag aat gga gac tgg     480
251 Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
252 145                 150                 155                 160
254 acc ttc cag acc ctg gtg atg ctg gaa aca gtt cct cga agt gga gag     528
255 Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
256                 165                 170                 175
258 gtt tac acc tgc caa gtg gag cac cca agc gtg aca agc cct ctc aca     576
259 Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
260                 180                 185                 190
262 gtg gaa tgg aga gca cgg tct gaa tct gca cag agc aag gtc gac gga     624
263 Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
264                 195                 200                 205
```

RAW SEQUENCE LISTING   DATE: 08/01/2000
PATENT APPLICATION: US/09/248,964   TIME: 13:05:48

Input Set : A:\HAR005.APP.app
Output Set: N:\CRF3\08012000\I248964.raw

```
266 ggt ggc ggc ggt cgc atc gcc cgg ctc gag gaa aaa gtg aaa acc ttg    672
267 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
268     210             215                 220
270 aaa gct cag aac tcg gag ctc gcg tcc acg gcc aac atg ctc agg gaa    720
271 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
272 225                 230                 235                 240
274 cag gtg gca cag ctt aaa cag aaa gtc atg aac cat tgagaattct atgac    771
275 Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
276                 245                 250
279 <210> SEQ ID NO: 4
280 <211> LENGTH: 252
281 <212> TYPE: PRT
282 <213> ORGANISM: Artificial Sequence
W--> 284 <220> FEATURE:
W--> 284 <223> OTHER INFORMATION:
284 <400> SEQUENCE: 4
285 Val Ser Leu Glu Lys Arg Glu Gly Asp Thr Arg Pro Arg Phe Leu Trp
286 1               5                   10                  15
288 Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
289             20                  25                  30
291 Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Ser Val Arg Phe Asp
292             35                  40                  45
294 Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
295     50                  55                  60
297 Ala Glu Tyr Trp Asn Ser Gln Lys Asp Ile Leu Glu Gln Ala Arg Ala
298 65                  70                  75                  80
300 Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser Phe
301             85                  90                  95
303 Thr Val Gln Arg Arg Val Gln Pro Lys Val Thr Val Tyr Pro Ser Lys
304             100                 105                 110
306 Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser Gly
307         115                 120                 125
309 Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Leu Asn Gly Gln Glu
310         130                 135                 140
312 Glu Lys Ala Gly Met Val Ser Thr Gly Leu Ile Gln Asn Gly Asp Trp
313 145                 150                 155                 160
315 Thr Phe Gln Thr Leu Val Met Leu Glu Thr Val Pro Arg Ser Gly Glu
316             165                 170                 175
318 Val Tyr Thr Cys Gln Val Glu His Pro Ser Val Thr Ser Pro Leu Thr
319             180                 185                 190
321 Val Glu Trp Arg Ala Arg Ser Glu Ser Ala Gln Ser Lys Val Asp Gly
322         195                 200                 205
324 Gly Gly Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu
325     210                 215                 220
327 Lys Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu
328 225                 230                 235                 240
330 Gln Val Ala Gln Leu Lys Gln Lys Val Met Asn His
331             245                 250
334 <210> SEQ ID NO: 5
```

VERIFICATION SUMMARY   DATE: 08/01/2000
PATENT APPLICATION: US/09/248,964   TIME: 13:05:49

Input Set : A:\HAR005.APP.app
Output Set: N:\CRF3\08012000\I248964.raw

```
L:131 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:131 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:284 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:284 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:580 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:580 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:872 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:872 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
```

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH
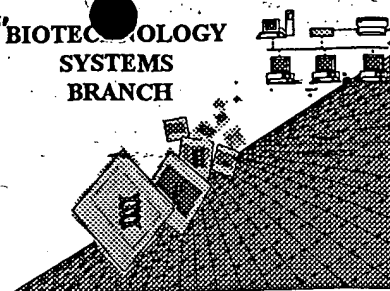
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/248,964*

Source: *1644*

Date Processed by STIC: *7/31/2000*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u> SERIAL NUMBER: _09/248,964_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) 2, 4 (more). Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An _initial_ or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An _initial_ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE